In the Description

Please replace the paragraph beginning at page 5, line 27, of the specification with the following rewritten paragraph.

- -The invention includes an isolated and purified polypeptide comprising the amino acid sequence of an ABACP polypeptide, wherein the polypeptide is encoded by a nucleic acid molecule that hybridizes under moderate or stringent conditions to a nucleic acid molecule in [SEQ ID NO:1 or 2], a degenerate form thereof or a complement. The invention includes a polypeptide comprising a sequence having greater than 70% sequence identity to a polypeptide of the invention. The polypeptide preferably comprises an ABACP polypeptide. The polypeptide is optionally isolated from *Arabidopsis thaliana*. The polypeptide preferably comprises a membrane spanning anchor domain including at least 70% sequence identity to the membrane spanning anchor domain of [SEQ ID NO.:3] and/or an heme binding domain including at least 70% sequence identity to the heme binding domain of [SEQ ID NO.:3].- -

Please replace the paragraph beginning at page 30, line 27, of the specification with the following rewritten paragraph.

- -7rb4 and was sequences using a pBR322 primer 5'ATTATCACATTAACC3' [SEQ ID NO.:4]. The primer is 60 bp away from the EcoRI site on this vector therefore the sequence read using this primer will be plant DNA. The sequence obtained from the right border rescue was 50bp of plant sequence and part of the NOS terminator. This was deemed insufficient to determine the identity of the site of insertion. The left border rescued plasmid was

sequenced using the same pBR322 primer and 460 bp of sequence obtained. Comparison of this sequence with *Arabidopsis* genomic DNA sequence database showed the left border of the T-DNA insert to be in the 2nd exon of a P450 monooxygenase located on chromosome II. Using a 173 bp Sal I/ BamHI fragment from 7lb3 to screen an *Arabidopsis* cDNA library, a partial cDNA clone was isolated and sequenced. The full-length cDNA was obtained by using gene specific primers and RT PCR. The forward gene specific primer used was (P45F151:5' TTGATCCGCCATGGCTACGAAACTCG3') [SEQ ID NO.:5], the reverse primer used was (P45R1976:5'TTAACTGCGCCTACGGCGCAATTTAG3') [SEQ ID NO.:6].- -

Please replace the paragraph beginning at page 38, line 15, of the specification with the following rewritten paragraph.

- -Although, F3 analysis strongly suggests that the T-DNA insertion is within approximately 1map unit from *cnr* 2-1, it does not prove that the *cnr* 2-1 mutation is caused by a T-DNA insertion disruption of the CYP 78 or CNR2. To demonstrate that the CNR2 causes the CO_2 non-responsive phenotype, a number of constructs were made using binary vectors and the full length cDNA of CYP78 (CNR2). The full-length cDNA was amplified by PCT using forward primer *Kpn*I/*Eco*RI P450F (5'-3': GGGTACCGAATTCATGGCTACGAAACTCGAAAGC) [SEQ ID NO.:7] and reverse primer *Hind*III/*Sac*I P450R (GCATAAGCTTGAGCTCTTAACTGCGCCTACGGCGCA) [SEQ ID NO.:8]. The amplification conditions were as follows: a single denaturing step at 94°C for two minutes preceded the 30 cycles of 30 seconds at 94°C; 60 seconds at 60°C; and a final elongation step at 72°C for 90 seconds. The resultant amplification product

was cloned into pGEM-T-EASY (Promega). The overexpression and antisense constructs were made in the following manner. The *Hind*III/*Xba*I fragment containing the 35S CaMV promoter from pBI221 was cloned into the respective sties in pBS (pBS-35S). For the anti-sense orientation, the CNR2 amplification product was digested with *Sac*I and *Eco* RI and ligated into the respective sites in pBS-35S to create pCNR2-AS. For the over-expression orientation, the CNR2 amplification product was digested with *Sac*I and *Kpn*I and inserted into the respective sites of pBS-35S to generate pCNR2-OV. To facilitate the insertion of the above constructs into a binary vector, pGPTV-ZERO was fitted with the pZERO-1 (Invitrogen) polylinker using *Hind*III and *XbaI* to generate pGPTV-ZERO. CNR2-OV was cloned in pGPTV-ZERO as a *Hind*III/*Eco*RI fragment. To examine the cellular localization of CNR2, another construct was made in pEGAD (a gift from S. Cutler) where the CNR2 amplification product was cloned in frame with the GFP downstream of the alanine flexi-linker region into the *Eco* RI/ *Hind*III cloning sites. Wild type *Arabidopsis* WS plants were transformed with the antisense construct, the overexpression construct and the pEGAD constructs [17].- -

REMARKS

The descriptive portion of the specification has been amended to include references to SEQ ID NOS.: 4 to 8. In addition, amendments of an editorial nature have been made.

Attached hereto is a marked-up version of the changes made by the present amendment to the claims and to the descriptive portion of the specification. The